SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of
     Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298
<151> 1999-06-03

<150> 09/701,536
<151> 2000-11-29

<150> 60/087,908
<151> 1998-06-04

<160> 31

<170> FastSEQ for Windows Version 4.0

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc   180
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gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
                  Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
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ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
         15                  20                  25


gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc     1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
     30                  35                  40


aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga     1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
 45                  50                  55                  60


gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag     1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
                 65                  70                  75


gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca     1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
                 80                  85                  90


gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat     1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
             95                  100                 105


gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg     1287
Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
     110                 115                 120


tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct     1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
125                 130                 135                 140


tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac     1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
                 145                 150                 155


tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc     1431
Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
                 160                 165                 170


tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc     1479
Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
             175                 180                 185


ctg ctg ttt gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc     1527
Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
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aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg       1575
Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
205             210             215                 220

gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca       1623
Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
                225             230             235

aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag       1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
            240             245             250

gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg       1719
Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
            255             260             265

gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat       1767
Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
            270             275             280

agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac       1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
285             290             295                 300

gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc       1863
Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
                305             310             315

tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc       1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
            320             325             330

aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac       1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
            335             340             345

cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt       2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
            350             355             360

aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac       2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
365             370             375             380

gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa       2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
                385             390             395

gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg       2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
            400             405             410

gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca       2199
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Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
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gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc       2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
    430             435             440

aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat       2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
445             450             455             460

cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag       2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys
                465             470             475

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct       2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala
                480             485             490

ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg       2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala
                495             500             505

aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc       2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser
            510             515             520

tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg       2535
Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala
525             530             535             540

agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc       2583
Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro
                545             550             555

ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa       2631
Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu
                560             565             570

ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag       2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln
                575             580             585

atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt       2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe
                590             595             600

tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca       2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
605             610             615             620

gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa       2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
                625             630             635
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gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga      2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
        640             645             650

atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg      2919
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
        655             660             665

ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca      2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
        670             675             680

ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa              3009
Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala *
685             690             695

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<210> 11
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
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      synthetic construct

<223> pCDJE 2-7

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Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
 1               5                   10                  15
Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
            20                  25                  30
Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
        35                  40                  45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
    50                  55                  60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65                  70                  75                  80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
                85                  90                  95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
            100                 105                 110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
        115                 120                 125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
        130                 135                 140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145                 150                 155                 160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
                165                 170                 175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
            180                 185                 190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
        195                 200                 205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
    210                 215                 220
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225                 230                 235                 240
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
            245                 250                 255
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
        260                 265                 270
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
        275                 280                 285
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305                 310                 315                 320
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
                325                 330                 335
Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
        340                 345                 350
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
        355                 360                 365
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
    370                 375                 380
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385                 390                 395                 400
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
                405                 410                 415
```

```
Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
        420                 425                 430
Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
        435                 440                 445
Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
        450                 455                 460
Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
465                 470                 475                 480
His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
                485                 490                 495
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
                500                 505                 510
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
                515                 520                 525
Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
        530                 535                 540
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545                 550                 555                 560
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
                565                 570                 575
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
                580                 585                 590
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
                595                 600                 605
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
        610                 615                 620
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625                 630                 635                 640
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
                645                 650                 655
Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
                660                 665                 670
Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
        675                 680                 685
Val Phe Leu Ala Thr Asn Val His Ala
    690                 695
```

```
<210> 12
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> misc_feature
<222> 1-46
<223> WN 466

<400> 12
cttggtaccc gtctcggcgc cgtgaccctc tcgaacttcc agggca              46
```

```
<210> 13
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> misc_feature
<222> 1-43
<223> CWN2444

<400> 13
agaggcactt gcacgtgcgg acttccgccg gcgaaaaaga aaa          43

<210> 14
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<223> JE Signal

<400> 14
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1               5                  10                  15
Val Val Ile Ala Cys Ala Gly Ala
            20

<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> CDS
<222> (911)...(2987)

<221> misc_feature
<222> (1)...(5308)
<223> pCBWN

<400> 15
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg    60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg   120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc   180
```

```
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt      480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
tcgctattac catggtgatg cggttttggc agtacatca atgggcgtgg atagcggttt      660
gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac      720
caaaatcaac gggactttcc aaaatgtcgt aacaactccg ccccattgac gcaaatgggc      780
ggtaggcgtg tacggtggga ggtctatata agcagagctc tctggctaac tagagaaccc      840
actgcttact ggcttatcga aattaatacg actcactata gggagaccca agcttggtac      900
cgccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg      949
              Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala
               1               5                   10

agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac      997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn
     15                  20                  25

ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat     1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp
 30                  35                  40                  45

gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga     1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg
                 50                  55                  60

gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc     1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys
                 65                  70                  75

cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc     1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys
             80                  85                  90

aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc     1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg
         95                  100                 105

cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa     1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu
110                 115                 120                 125

agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc     1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala
                 130                 135                 140

aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga     1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly
             145                 150                 155
```

```
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc    1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr
        160                 165                 170

atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct    1477
Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala
        175                 180                 185

tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga    1525
Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly
190                 195                 200                 205

gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc    1573
Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys
                210                 215                 220

gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg    1621
Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met
                225                 230                 235

aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg    1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu
                240                 245                 250

gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga    1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly
        255                 260                 265

gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa    1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln
270                 275                 280                 285

gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa    1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
                290                 295                 300

gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata    1861
Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile
                305                 310                 315

gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt    1909
Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe
        320                 325                 330

gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag    1957
Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln
        335                 340                 345

gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct    2005
Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro
350                 355                 360                 365

tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt    2053
```

```
Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys
            370                 375                 380
```

```
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt    2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val
            385                 390                 395
```

```
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac    2149
Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn
            400                 405                 410
```

```
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg    2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr
            415                 420                 425
```

```
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca    2245
Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala
430                 435                 440                 445
```

```
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att    2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile
            450                 455                 460
```

```
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg    2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu
            465                 470                 475
```

```
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat    2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr
            480                 485                 490
```

```
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca    2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr
            495                 500                 505
```

```
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga    2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly
510                 515                 520                 525
```

```
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg    2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr
            530                 535                 540
```

```
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg    2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr
            545                 550                 555
```

```
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca    2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser
            560                 565                 570
```

```
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac    2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His
            575                 580                 585
```

```
aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga      2725
Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly
590             595             600                 605

gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca      2773
Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser
                610             615             620

gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc      2821
Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe
            625             630             635

gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa      2869
Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln
            640             645             650

gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat      2917
Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp
    655             660             665

agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc      2965
Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe
670             675             680             685

ctc tcc gtg aac gtg cac gcc t gaaggcggcc gctcgagcat gcatctagag       3017
Leu Ser Val Asn Val His Ala
                690

ggccctattc tatagtgtca cctaaatgct agagctcgct gatcagcctc gactgtgcct    3077
tctagttgcc agccatctgt tgtttgcccc tccccgtgc cttccttgac cctggaaggt     3137
gccactccca ctgtcctttc ctaataaaat gaggaaattg catcgcattg tctgagtagg    3197
tgtcattcta ttctgggggg tggggtgggg caggacagca aggggagga ttgggaagac     3257
aatagcaggc atgctgggga tgcggtgggc tctatggctt ctgaggcgga aagaaccagc    3317
tgcattaatg aatcggccaa cgcgcgggga gaggcggttt gcgtattggg cgctcttccg    3377
cttcctcgct cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc    3437
actcaaaggc ggtaatacgg ttatccacag aatcaggga taacgcagga aagaacatgt     3497
gagcaaaagg ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgttttttcc   3557
ataggctccg cccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa    3617
acccgacagg actataaaga taccaggcgt ttccccctgg aagctccctc gtgcgctctc    3677
ctgttccgac cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg    3737
cgctttctca tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc    3797
tgggctgtgt gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc    3857
gtcttgagtc caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca    3917
ggattagcag agcgaggtat gtaggcggtg ctacagagtt cttgaagtgg tggcctaact    3977
acggctacac tagaagaaca gtatttggta tctgcgctct gctgaagcca gttaccttcg    4037
gaaaaagagt tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt    4097
ttgtttgcaa gcagcagatt acgcgcagaa aaaaggatc tcaagaagat cctttgatct     4157
tttctacggg gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatga    4217
gattatcaaa aaggatcttc acctagatcc ttttaaatta aaaatgaagt tttaaatcaa    4277
tctaaagtat atatgagtaa acttggtctg acagttacca atgcttaatc agtgaggcac    4337
ctatctcagc gatctgtcta tttcgttcat ccatagttgc ctgactcccc gtcgtgtaga    4397
taactacgat acgggagggc ttaccatctg gccccagtgc tgcaatgata ccgcgagacc    4457
cacgctcacc ggctccagat ttatcagcaa taaaccagcc agccggaagg gccgagcgca    4517
```

```
gaagtggtcc tgcaacttta tccgcctcca tccagtctat taattgttgc cgggaagcta    4577
gagtaagtag ttcgccagtt aatagtttgc gcaacgttgt tgccattgct acaggcatcg    4637
tggtgtcacg ctcgtcgttt ggtatggctt cattcagctc cggttcccaa cgatcaaggc    4697
gagttacatg atcccccatg ttgtgcaaaa aagcggttag ctccttcggt cctccgatcg    4757
ttgtcagaag taagttggcc gcagtgttat cactcatggt tatggcagca ctgcataatt    4817
ctcttactgt catgccatcc gtaagatgct tttctgtgac tggtgagtac tcaaccaagt    4877
cattctgaga atagtgtatg cggcgaccga gttgctcttg cccggcgtca atacgggata    4937
ataccgcgcc acatagcaga actttaaaag tgctcatcat tggaaaacgt tcttcggggc    4997
gaaaactctc aaggatctta ccgctgttga gatccagttc gatgtaaccc actcgtgcac    5057
ccaactgatc ttcagcatct tttactttca ccagcgtttc tgggtgagca aaaacaggaa    5117
ggcaaaatgc cgcaaaaaag gaataaggg cgacacggaa atgttgaata ctcatactct    5177
tcctttttca atattattga agcatttatc agggttattg tctcatgagc ggatacatat    5237
ttgaatgtat ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc    5297
cacctgacgt c                                                        5308
```

<210> 16
<211> 692
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<223> pCBWN

<400> 16

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15
Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
            20                  25                  30
Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
        35                  40                  45
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
    50                  55                  60
Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65                  70                  75                  80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
                85                  90                  95
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
            100                 105                 110
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
        115                 120                 125
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
    130                 135                 140
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145                 150                 155                 160
Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
                165                 170                 175
Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
                180                 185                 190
Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
            195                 200                 205
```

```
Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
    210                 215                 220
Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
225                 230                 235                 240
Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
                245                 250                 255
Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
                260                 265                 270
Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
        275                 280                 285
Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
    290                 295                 300
Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
305                 310                 315                 320
Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
                325                 330                 335
Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
                340                 345                 350
Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
                355                 360                 365
Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
    370                 375                 380
Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
385                 390                 395                 400
Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
                405                 410                 415
Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
                420                 425                 430
Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
            435                 440                 445
Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
    450                 455                 460
Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
465                 470                 475                 480
Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
                485                 490                 495
Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
            500                 505                 510
Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
            515                 520                 525
Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
    530                 535                 540
Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
545                 550                 555                 560
Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
                565                 570                 575
Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
            580                 585                 590
Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
            595                 600                 605
Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
    610                 615                 620
Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625                 630                 635                 640
```

```
Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
            645                 650                 655
Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
            660                 665                 670
Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
            675                 680                 685
Asn Val His Ala
            690
```

<210> 17
<211> 5334
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> CDS
<222> (916)...(3007)

<221> misc_feature
<222> (1)...(5334)
<223> pCBJE 1-14

<400> 17
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gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg       60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt      480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg      780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc      900
tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
                  Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
                   1               5                  10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
         15                  20                  25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc     1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
      30                  35                  40
```

```
aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga    1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
 45                  50                  55                  60

gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag    1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
                 65                  70                  75

gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca    1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
             80                  85                  90

gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat    1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
         95                  100                 105

gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg    1287
Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
     110                 115                 120

tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct    1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
125                 130                 135                 140

tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac    1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
                 145                 150                 155

tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc    1431
Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
             160                 165                 170

tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc    1479
Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
         175                 180                 185

ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc    1527
Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
     190                 195                 200

aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg    1575
Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
205                 210                 215                 220

gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca    1623
Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
                 225                 230                 235

aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag    1671
Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
             240                 245                 250

gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg    1719
```

```
Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
    255             260             265

gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat      1767
Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
    270             275             280

agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac      1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
285             290             295             300

gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc      1863
Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
            305             310             315

tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc      1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
            320             325             330

aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac      1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
            335             340             345

cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt      2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
    350             355             360

aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac      2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
365             370             375             380

gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa      2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
            385             390             395

gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg      2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
            400             405             410

gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca      2199
Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
            415             420             425

gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc      2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
    430             435             440

aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat      2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
445             450             455             460

cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag      2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys
            465             470             475
```

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct   2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala
            480   485   490

ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg   2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala
            495   500   505

aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc   2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser
            510   515   520

tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg   2535
Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala
525   530   535   540

agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc   2583
Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro
                545   550   555

ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa   2631
Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu
                560   565   570

ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag   2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln
                575   580   585

atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt   2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe
            590   595   600

tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca   2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
605   610   615   620

gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa   2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
                625   630   635

gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga   2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
                640   645   650

atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg   2919
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
                655   660   665

ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca   2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
            670   675   680

ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct t aattagtttg   3017

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
685   690   695

```
agcggccgct cgagcatgca tctagagggc cctattctat agtgtcacct aaatgctaga   3077
gctcgctgat cagcctcgac tgtgccttct agttgccagc catctgttgt ttgcccctcc   3137
cccgtgcctt ccttgaccct ggaaggtgcc actcccactg tcctttccta ataaaatgag   3197
gaaattgcat cgcattgtct gagtaggtgt cattctattc tggggggtgg ggtggggcag   3257
gacagcaagg gggaggattg ggaagacaat agcaggcatg ctggggatgc ggtgggctct   3317
atggcttctg aggcggaaag aaccagctgc attaatgaat cggccaacgc gcggggagag   3377
gcggtttgcg tattgggcgc tcttccgctt cctcgctcac tgactcgctg cgctcggtcg   3437
ttcggctgcg gcgagcggta tcagctcact caaaggcggt aatacggtta tccacagaat   3497
caggggataa cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta   3557
aaaaggccgc gttgctggcg tttttccata ggctccgccc ccctgacgag catcacaaaa   3617
atcgacgctc aagtcagagg tggcgaaacc cgacaggact ataaagatac caggcgtttc   3677
cccctggaag ctccctcgtg cgctctcctg ttccgaccct gccgcttacc ggatacctgt   3737
ccgcctttct cccttcggga agcgtggcgc tttctcatag ctcacgctgt aggtatctca   3797
gttcggtgta ggtcgttcgc tccaagctgg gctgtgtgca cgaaccccccc gttcagcccg   3857
accgctgcgc cttatccggt aactatcgtc ttgagtccaa cccggtaaga cacgacttat   3917
cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta ggcggtgcta   3977
cagagttctt gaagtggtgg cctaactacg gctacactag aagaacagta tttggtatct   4037
gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga tccggcaaac   4097
aaaccaccgc tggtagcggt ggtttttttg tttgcaagca gcagattacg cgcagaaaaa   4157
aaggatctca agaagatcct ttgatctttt ctacggggtc tgacgctcag tggaacgaaa   4217
actcacgtta agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatccttt   4277
taaattaaaa atgaagtttt aaatcaatct aaagtatata tgagtaaact tggtctgaca   4337
gttaccaatg cttaatcagt gaggcaccta tctcagcgat ctgtctattt cgttcatcca   4397
tagttgcctg actccccgtc gtgtagataa ctacgatacg ggagggctta ccatctggcc   4457
ccagtgctgc aatgataccg cgagacccac gctcaccggc tccagattta tcagcaataa   4517
accagccagc cggaagggcc gagcgcagaa gtggtcctgc aactttatcc gcctccatcc   4577
agtctattaa ttgttgccgg gaagctagag taagtagttc gccagttaat agtttgcgca   4637
acgttgttgc cattgctaca ggcatcgtgg tgtcacgctc gtcgtttggt atggcttcat   4697
tcagctccgg ttcccaacga tcaaggcgag ttacatgatc ccccatgttg tgcaaaaaag   4757
cggttagctc cttcggtcct ccgatcgttg tcagaagtaa gttggccgca gtgttatcac   4817
tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta agatgctttt   4877
ctgtgactgg tgagtactca accaagtcat tctgagaata gtgtatgcgg cgaccgagtt   4937
gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact ttaaaagtgc   4997
tcatcattgg aaaacgttct cggggcgaa aactctcaag gatcttaccg ctgttgagat   5057
ccagttcgat gtaacccact cgtgcaccca actgatcttc agcatctttt actttcacca   5117
gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataagggcga   5177
cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg   5237
gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg   5297
ttccgcgcac atttccccga aaagtgccac ctgacgt                            5334
```

<210> 18
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<223> pCBJE 1-14

```
<400> 18
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
 1               5                  10                  15
Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
            20                  25                  30
Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
            35                  40                  45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
    50                  55                  60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65                  70                  75                  80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
                85                  90                  95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
            100                 105                 110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
            115                 120                 125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
            130                 135                 140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145                 150                 155                 160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
                165                 170                 175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
            180                 185                 190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
            195                 200                 205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
    210                 215                 220
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225                 230                 235                 240
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
                245                 250                 255
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
            260                 265                 270
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
            275                 280                 285
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
            290                 295                 300
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305                 310                 315                 320
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
                325                 330                 335
Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
            340                 345                 350
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
            355                 360                 365
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
    370                 375                 380
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385                 390                 395                 400
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
                405                 410                 415
```

```
Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
        420             425             430
Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
        435             440             445
Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
    450             455             460
Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
465             470             475             480
His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
            485             490             495
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
        500             505             510
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
        515             520             525
Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
    530             535             540
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545             550             555             560
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
            565             570             575
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
        580             585             590
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
    595             600             605
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
    610             615             620
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625             630             635             640
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
            645             650             655
Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
        660             665             670
Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
    675             680             685
Val Phe Leu Ala Thr Asn Val His Ala
690             695
```

<210> 19
<211> 5283
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> CDS
<222> (910)...(2965)

<400> 19
```
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240
```

```
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata    300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc    360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc    420
attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt    480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt    540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca    600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg    660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc    720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg    780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca    840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc    900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc    951
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
             1               5                   10
```

```
ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac     999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp
 15               20                  25                      30
```

```
agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc    1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser
                  35                  40                  45
```

```
cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg    1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met
              50                  55                  60
```

```
gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac    1143
Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp
          65                  70                  75
```

```
cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat    1191
Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp
      80                  85                  90
```

```
agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg    1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg
 95               100                 105                 110
```

```
ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc    1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val
                  115                 120                 125
```

```
ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc    1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val
              130                 135                 140
```

```
acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc    1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala
          145                 150                 155
```

```
att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg    1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val
      160                 165                 170
```

```
act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg     1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg
175             180             185             190

tgc acg cat ctt gag aac aga gat ttt gtg aca gga act caa ggg acc     1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr
                195             200             205

acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca     1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr
            210             215             220

gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag     1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln
            225             230             235

gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc     1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr
            240             245             250

aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt     1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu
255             260             265             270

ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac     1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp
                275             280             285

cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg     1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val
            290             295             300

gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac     1863
Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His
            305             310             315

gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac     1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His
            320             325             330

aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca     1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser
335             340             345             350

gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac     2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp
                355             360             365

tat gga gat gtg tcg ctg acg tgt aaa gtg gca agt ggg att gat gtc     2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val
            370             375             380

gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct     2103
```

```
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro
        385                 390                 395

tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc      2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro
        400                 405                 410

tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg      2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val
415                 420                 425                 430

gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg      2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly
                435                 440                 445

gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc      2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala
            450                 455                 460

agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt      2343
Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys
            465                 470                 475

gat gtg gga ctg gaa aag ctg aaa ctg aaa ggc aca acc tac tcc atg      2391
Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met
        480                 485                 490

tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc      2439
Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly
495                 500                 505                 510

cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca      2487
His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro
                515                 520                 525

tgt cgg atc ccg gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat      2535
Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn
            530                 535                 540

gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc      2583
Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly
            545                 550                 555

gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg      2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val
        560                 565                 570

gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga      2679
Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg
575                 580                 585                 590

atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga      2727
Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly
                595                 600                 605
```

```
gaa cat gca tgg gac ttt ggc tca gta ggc ggg gta ctg tct tct gtg    2775
Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val
            610             615                 620


ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt    2823
Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe
            625                 630                 635


ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc    2871
Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val
            640                 645                 650


tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt    2919
Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu
655                 660                 665                 670


gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca t      2965
Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala
                675                 680                 685


gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag    3025
agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc    3085
ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct aataaaatga    3145
ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctggggggtg gggtggggca    3205
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tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta agatgctttt    4825
ctgtgactgg tgagtactca accaagtcat tctgagaata gtgtatgcgg cgaccgagtt    4885
gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact ttaaaagtgc    4945
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```
tcatcattgg aaaacgttct tcggggcgaa aactctcaag gatcttaccg ctgttgagat    5005
ccagttcgat gtaacccact cgtgcaccca actgatcttc agcatctttt actttcacca    5065
gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataagggcga    5125
cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg    5185
gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg    5245
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<210> 20
<211> 681
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<400> 20
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Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
            20                  25                  30
Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
        35                  40                  45
Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
    50                  55                  60
Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65                  70                  75                  80
Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
                85                  90                  95
Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
            100                 105                 110
Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
        115                 120                 125
Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
    130                 135                 140
Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145                 150                 155                 160
Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
            165                 170                 175
Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
            180                 185                 190
Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
        195                 200                 205
Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
    210                 215                 220
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225                 230                 235                 240
Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
            245                 250                 255
Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
            260                 265                 270
Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
        275                 280                 285
```

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```
Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
    290                 295                 300
Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305                 310                 315                 320
Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
                325                 330                 335
Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
                340                 345                 350
Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
                355                 360                 365
Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
    370                 375                 380
Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
385                 390                 395                 400
Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
                405                 410                 415
His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
                420                 425                 430
Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
                435                 440                 445
Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
    450                 455                 460
His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
465                 470                 475                 480
Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
                485                 490                 495
Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
                500                 505                 510
Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
    515                 520                 525
Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
    530                 535                 540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545                 550                 555                 560
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
                565                 570                 575
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
                580                 585                 590
Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
                595                 600                 605
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
    610                 615                 620
Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625                 630                 635                 640
Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
                645                 650                 655
Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
                660                 665                 670
Met Phe Leu Ser Leu Gly Val Gly Ala
    675                 680
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<210> 21
<211> 5304
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> CDS
<222> (910)...(2986)

<400> 21
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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc     360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc     420
attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt     480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt     540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca     600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg     660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc     720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg     780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca     840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc     900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc     951
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
             1               5                  10

ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat     999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
 15                  20                  25                  30

cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc    1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
                 35                  40                  45

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct    1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
             50                  55                  60

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca    1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
         65                  70                  75

gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac    1191
Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp
     80                  85                  90

gtc gaa gag gtg tgg gtg cac tac ggc aga tgc acg cgc atg gga cat    1239
Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His
 95                  100                 105                 110

tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc    1287
```

```
Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser
            115             120             125


aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc     1335
Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr
            130             135             140


aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat     1383
Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr
            145             150             155


gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca     1431
Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr
            160             165             170


cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac     1479
Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr
175             180             185             190


agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc     1527
Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala
            195             200             205


agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc     1575
Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val
            210             215             220


aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag     1623
Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys
            225             230             235


atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca     1671
Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala
            240             245             250


acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa     1719
Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu
255             260             265             270


gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat     1767
Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp
            275             280             285


gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg     1815
Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
            290             295             300


agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg     1863
Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly
            305             310             315


aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg     1911
Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val
            320             325             330
```

```
cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att    1959
His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile
335             340             345                 350

gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc    2007
Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser
                355             360             365

ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa    2055
Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu
            370             375             380

gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag    2103
Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys
        385             390             395

gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt    2151
Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu
    400             405             410

cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg    2199
Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu
415             420             425             430

gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta    2247
Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu
            435             440             445

gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca    2295
Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro
        450             455             460

gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa    2343
Ala Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys
        465             470             475

tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc    2391
Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly
        480             485             490

atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg    2439
Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly
495             500             505             510

cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc    2487
His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro
            515             520             525

tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg    2535
Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro
        530             535             540

gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg    2583
```

```
Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala
        545                 550                 555
```

```
aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac    2631
Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr
        560                 565                 570
```

```
atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa    2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys
575                 580                 585                 590
```

```
gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc    2727
Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala
                595                 600                 605
```

```
caa cgg cta gcc gtc tta ggg gac aca gcg tgg gac ttt gga tct att    2775
Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile
                610                 615                 620
```

```
gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga    2823
Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly
                625                 630                 635
```

```
gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg    2871
Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly
        640                 645                 650
```

```
cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg    2919
Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg
655                 660                 665                 670
```

```
agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg    2967
Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu
                675                 680                 685
```

```
gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg    3016
Ala Thr Ser Val Gln Ala
                690
```

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ccctattcta tagtgtcacc taaatgctag agctcgctga tcagcctcga ctgtgccttc    3076
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cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc tgagtaggtg    3196
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gctgtgtgca cgaacccccc gttcagcccg accgctgcgc cttatccggt aactatcgtc    3856
ttgagtccaa cccggtaaga cacgacttat cgccactggc agcagccact ggtaacagga    3916
```

```
ttagcagagc gaggtatgta ggcggtgcta cagagttctt gaagtggtgg cctaactacg    3976
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aaagagttgg tagctcttga tccggcaaac aaaccaccgc tggtagcggt ggtttttttg    4096
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ctacggggtc tgacgctcag tggaacgaaa actcacgtta agggattttg gtcatgagat    4216
tatcaaaaag gatcttcacc tagatccttt taaattaaaa atgaagtttt aaatcaatct    4276
aaagtatata tgagtaaact tggtctgaca gttaccaatg cttaatcagt gaggcaccta    4336
tctcagcgat ctgtctattt cgttcatcca tagttgcctg actccccgtc gtgtagataa    4396
ctacgatacg ggagggctta ccatctggcc ccagtgctgc aatgataccg cgagacccac    4456
gctcaccggc tccagattta tcagcaataa accagccagc cggaagggcc gagcgcagaa    4516
gtggtcctgc aactttatcc gcctccatcc agtctattaa ttgttgccgg gaagctagag    4576
taagtagttc gccagttaat agtttgcgca acgttgttgc cattgctaca ggcatcgtgg    4636
tgtcacgctc gtcgtttggt atggcttcat tcagctccgg ttcccaacga tcaaggcgag    4696
ttacatgatc ccccatgttg tgcaaaaaag cggttagctc cttcggtcct ccgatcgttg    4756
tcagaagtaa gttggccgca gtgttatcac tcatggttat ggcagcactg cataattctc    4816
ttactgtcat gccatccgta agatgctttt ctgtgactgg tgagtactca accaagtcat    4876
tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc ggcgtcaata cgggataata    4936
ccgcgccaca tagcagaact ttaaaagtgc tcatcattgg aaaacgttct cggggcgaa     4996
aactctcaag atcttaccg ctgttgagat ccagttcgat gtaacccact cgtgcaccca     5056
actgatcttc agcatctttt actttcacca gcgtttctgg gtgagcaaaa acaggaaggc     5116
aaaatgccgc aaaaaaggga ataagggcga cacggaaatg ttgaatactc atactcttcc     5176
tttttcaata ttattgaagc atttatcagg gttattgtct catgagcgga tacatatttg     5236
aatgtattta gaaaaataaa caaatagggg ttccgcgcac atttccccga aaagtgccac     5296
ctgacgtc                                                             5304
```

<210> 22
<211> 692
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<400> 22

```
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15
Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
            20                  25                  30
Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
        35                  40                  45
Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
        50                  55                  60
Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65                  70                  75                  80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
                85                  90                  95
Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
            100                 105                 110
Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
        115                 120                 125
Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
        130                 135                 140
```

```
Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145                 150                 155                 160
Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
                165                 170                 175
Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
            180                 185                 190
Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
        195                 200                 205
Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
    210                 215                 220
Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
225                 230                 235                 240
Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
                245                 250                 255
Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
            260                 265                 270
Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
        275                 280                 285
Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
    290                 295                 300
Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
305                 310                 315                 320
Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
                325                 330                 335
Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
            340                 345                 350
Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
        355                 360                 365
Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
    370                 375                 380
Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
385                 390                 395                 400
Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
                405                 410                 415
Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
            420                 425                 430
Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
        435                 440                 445
Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
    450                 455                 460
Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
465                 470                 475                 480
Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
                485                 490                 495
Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
        500                 505                 510
Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
        515                 520                 525
Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
    530                 535                 540
Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
545                 550                 555                 560
Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
                565                 570                 575
```

```
Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
          580                   585                   590
Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
          595                   600                   605
Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
    610                   615                   620
Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625                   630                   635                   640
Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
                  645                   650                   655
Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
              660                   665                   670
Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
          675                   680                   685
Ser Val Gln Ala
          690


<210> 23
<211> 5271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> CDS
<222> (910)...(2953)

<400> 23
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120
cgagcaaaat ttaagctaca caaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc     360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc     420
attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt     480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt     540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca     600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg     660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc     720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg     780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca     840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc     900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc     951
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
             1               5                   10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa     999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
  15                  20                  25                  30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca    1047
```

```
Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr
            35                  40                  45


ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag    1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys
            50                  55                  60


tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca    1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro
            65                  70                  75


aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac    1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn
        80                  85                  90


gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg    1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg
95                  100                 105                 110


tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag    1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys
            115                 120                 125


acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc    1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu
            130                 135                 140


caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg    1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr
            145                 150                 155


gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc    1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val
        160                 165                 170


gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac    1479
Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His
175                 180                 185                 190


tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga    1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly
            195                 200                 205


act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg    1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met
            210                 215                 220


gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att    1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile
            225                 230                 235


gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act    1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr
        240                 245                 250
```

```
cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta        1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu
255             260             265                 270

gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat        1767
Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp
                275             280             285

aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg        1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val
            290             295             300

gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt        1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val
        305             310             315

gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg        1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly
        320             325             330

gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat        1959
Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp
335             340             345             350

gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct        2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala
                355             360             365

aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac        2055
Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr
            370             375             380

atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc        2103
Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala
            385             390             395

cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga        2151
Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg
        400             405             410

gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc        2199
Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile
415             420             425             430

aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt        2247
Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu
            435             440             445

act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac        2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr
            450             455             460

aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg        2343
```

```
Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu
        465                 470                 475
```

```
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt      2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe
        480                 485                 490
```

```
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg      2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val
495                 500                 505                 510
```

```
aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat      2487
Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp
                515                 520                 525
```

```
gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc      2535
Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro
                530                 535                 540
```

```
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct      2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro
                545                 550                 555
```

```
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act      2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr
        560                 565                 570
```

```
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag      2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln
575                 580                 585                 590
```

```
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg      2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp
                595                 600                 605
```

```
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att      2775
Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile
                610                 615                 620
```

```
cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac      2823
His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn
                625                 630                 635
```

```
tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc      2871
Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile
        640                 645                 650
```

```
aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg      2919
Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val
655                 660                 665                 670
```

```
atc atg atg ttt ttg tct cta gga gtt ggg gcg t gagcggccgc            2963
Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala
        675                 680
```

```
tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag agctcgctga   3023
tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgtgcct   3083
tccttgaccc tggaaggtgc cactcccact gtcctttcct aataaaatga ggaaattgca   3143
tcgcattgtc tgagtaggtg tcattctatt ctggggggtg gggtggggca ggacagcaag   3203
ggggaggatt gggaagacaa tagcaggcat gctggggatg cggtgggctc tatggcttct   3263
gaggcggaaa gaacagctgc attaatgaat cggccaacgc gcggggagag gcggtttgcg   3323
tattgggcgc tcttccgctt cctcgctcac tgactcgctg cgctcggtcg ttcggctgcg   3383
gcgagcggta tcagctcact caaaggcggt aatacggtta ccacagaat cagggggataa   3443
cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc   3503
gttgctggcg ttttttccata ggctccgccc ccctgacgag catcacaaaa atcgacgctc   3563
aagtcagagg tggcgaaacc cgacaggact ataaagatac caggcgtttc ccccctggaag  3623
ctccctcgtg cgctctcctg ttccgaccct gccgcttacc ggatacctgt ccgcctttct   3683
cccttcggga agcgtggcgc tttctcaatg ctcacgctgt aggtatctca gttcggtgta   3743
ggtcgttcgc tccaagctgg gctgtgtgca cgaacccccc gttcagcccg accgctgcgc   3803
cttatccggt aactatcgtc ttgagtccaa cccggtaaga cacgacttat cgccactggc   3863
agcagccact ggtaacagga ttagcagagc gaggtatgta ggcggtgcta cagagttctt   3923
gaagtggtgg cctaactacg gctacactag aaggacagta tttggtatct gcgctctgct   3983
gaagccagtt accttcggaa aaagagttgg tagctcttga tccggcaaac aaaccaccgc   4043
tggtagcggt ggtttttttg tttgcaagca gcagattacg cgcagaaaaa aaggatctca   4103
agaagatcct ttgatctttt ctacggggtc tgacgctcag tggaacgaaa actcacgtta   4163
agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatccttt taaattaaaa   4223
atgaagtttt aaatcaatct aaagtatata tgagtaaact tggtctgaca gttaccaatg   4283
cttaatcagt gaggcaccta tctcagcgat ctgtctattt cgttcatcca tagttgcctg   4343
actccccgtc gtgtagataa ctacgatacg ggagggctta ccatctggcc ccagtgctgc   4403
aatgataccg cgagacccac gctcaccggc tccagattta tcagcaataa accagccagc   4463
cggaagggcc gagcgcagaa gtggtcctgc aactttatcc gcctccatcc agtctattaa   4523
ttgttgccgg gaagctagag taagtagttc gccagttaat agtttgcgca acgttgttgc   4583
cattgctaca ggcatcgtgg tgtcacgctc gtcgtttggt atggcttcat tcagctccgg   4643
ttcccaacga tcaaggcgag ttacatgatc ccccatgttg tgcaaaaaag cggttagctc   4703
cttcggtcct ccgatcgttg tcagaagtaa gttggccgca gtgttatcac tcatggttat   4763
ggcagcactg cataattctc ttactgtcat gccatccgta agatgctttt ctgtgactgg   4823
tgagtactca accaagtcat tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc   4883
ggcgtcaata cgggataata ccgcgccaca tagcagaact ttaaaagtgc tcatcattgg   4943
aaaacgttct cggggcgaa aactctcaag gatcttaccg ctgttgagat ccagttcgat   5003
gtaacccact cgtgcaccca actgatcttc agcatctttt actttcacca gcgtttctgg   5063
gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga taagggcga cacggaaatg   5123
ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg gttattgtct   5183
catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg ttccgcgcac   5243
atttccccga aaagtgccac ctgacgtc                                       5271
```

<210> 24
<211> 681
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<400> 24
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

```
Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
        20                  25                  30
Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
        35                  40                  45
Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
        50                  55                  60
Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65                  70                  75                  80
Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
                85                  90                  95
Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
            100                 105                 110
Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
            115                 120                 125
Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
        130                 135                 140
Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145                 150                 155                 160
Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
            165                 170                 175
Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
            180                 185                 190
Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
            195                 200                 205
Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
        210                 215                 220
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225                 230                 235                 240
Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
            245                 250                 255
Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
            260                 265                 270
Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
        275                 280                 285
Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
        290                 295                 300
Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305                 310                 315                 320
Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
            325                 330                 335
Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
            340                 345                 350
Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
            355                 360                 365
Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
370                 375                 380
Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
385                 390                 395                 400
Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
            405                 410                 415
His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
            420                 425                 430
Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
        435                 440                 445
```

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```
Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
    450                 455                 460
His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
465                 470                 475                 480
Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
                485                 490                 495
Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
            500                 505                 510
Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
        515                 520                 525
Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
    530                 535                 540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545                 550                 555                 560
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
                565                 570                 575
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
            580                 585                 590
Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
        595                 600                 605
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
    610                 615                 620
Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625                 630                 635                 640
Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
                645                 650                 655
Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
            660                 665                 670
Met Phe Leu Ser Leu Gly Val Gly Ala
        675                 680
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<210> 25
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> misc_feature
<222> 1-35
<223> POW 454

<400> 25
aaaagaaaaa gcgctaccac catccaccgg gacag   35

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of artificial sequence; note =
      synthetic construct

<221> misc_feature
<222> 1-41
<223> CPOW 2417

<400> 26
actgttaccc tcaaccccgt actcgccggc gaaaaagaaa a                          41

<210> 27
<211> 24
<212> PRT
<213> Artificial Sequence


<220>
<223> Description of artificial sequence; note =
      synthetic construct

<223> Modified JE Signal

<400> 27
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1               5                   10                  15
Val Val Ile Ala Gly Thr Ser Ala
            20

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of artificial sequence; note =
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<221> misc_feature
<222> 1-36
<223> YF 482

<400> 28
aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac                                36

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of artificial sequence; note =
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<221> misc_feature
<222> 1-41
<223> CYF 2433

<400> 29
acagagatcc tcaaccccgc actcgccggc gaaaaagaaa a                    41


<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
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<221> misc_feature
<222> 1-41
<223> SLE 463

<400> 30
aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a                    41


<210> 31
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
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<221> misc_feature
<222> 1-40
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaaagaaa                      40
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